

PATRICK TYLER GARRETT

✉ contact@pgarrett.dev • 🌐 pgarrett.dev • 🆔 0000-0002-8434-9693 • 📄 Google Scholar • 📁 pgarrett-scripps

Bioinformatics Ph.D. candidate and scientific software engineer focused on mass spectrometry-based proteomics. I build high-performance, open-source Python and Rust libraries (database/spectral search, raw and mzml I/O, and ProForma-compliant peptidoform tooling) and train deep-learning models for peptide property prediction. Creator of the open-source tacular-omics ecosystem.

SKILLS

Languages: Python (Polars, pandas, Numba, sklearn), Rust (PyO3, maturin, rayon)

Proteomics: DDA Search (Sage, ProLuCID), DIA Search (DIA-NN), Bruker timsTOF data (PRM, DDA, DIA), mzML, PSI Formats (ProForma, mzPaf, mzML, mzIdentML, mzTab), PTM ontologies (PSI-MOD, Unimod, UniProt PTM), Quantitative analysis (LFQ, TMT, SILAC, CPP)

Machine Learning: Deep learning (Keras, Transformers, RNN, CNN), Traditional ML (SKlearn, Xgboost), Fine-tuning, parameter search, and hyperparameter optimization

Other: Git, GitHub, GitHub Actions, CI/CD, Docker, Proxmox, Containers, Networking, Linux, HPC, Slurm, Claude code, Skills, MCP, LangGraph

EXPERIENCE

Graduate Researcher

2021–Present

Yates Laboratory, Scripps Research, La Jolla, CA

- Conduct doctoral research in mass spectrometry-based proteomics under John R. Yates III.
- Design Smart Acquisition Methods (SAMS) for Bruker timsTOF instruments, including hybrid DDA/PRM acquisition strategies driven by real-time database search.

Research Technician

2019–2021

Yates Laboratory, Scripps Research, La Jolla, CA

- Developed a real-time search pipeline with Bruker Daltonics that enabled bidirectional communication between the timsTOF Pro PASEF API and the ProLuCID GPU search engine, supporting real-time decision-making during acquisition.
- Trained deep learning models for peptide property prediction (collisional cross-section, retention time, fragmentation) deployed inside the PaSER pipeline, including a mixture density network for peptide CCS distributions.

Programmer (Summer Internship)

2019–2020

SPAWAR / NAVWAR, San Diego, CA

- Built an automated network test environment using the Robot Framework, Python, and bash on a small development team within a classified lab environment.
- Owned scripting, bug triage, and system testing; contributed to network automation tooling and release processes.

SELECTED SOFTWARE

tacular-omics: A permissively licensed Python ecosystem for computational proteomics, spanning peptidoform manipulation, spectral search, instrument I/O, and modification ontologies. `peptacular`, `spxtacular`, `spectrl`, `sequoia-boost`, `sage-plus`, `rustypaper`

EDUCATION

Ph.D. Candidate in Bioinformatics

2021–Expected Fall 2026

Scripps Research Skaggs Graduate School, La Jolla, CA

B.S. in Cognitive Science

2016–2020

University of California, San Diego, La Jolla, CA

SELECTED PUBLICATIONS

Garrett PT, et al. dnoise: Fast, In-Place Denoising of Bruker timsTOF Data with an Ion-Mobility Streak Filter. *bioRxiv / Journal of the American Society for Mass Spectrometry*, 2026

Turner NP, ..., **Garrett PT**, et al. Rapid Histone Post-Translational Modification Analysis Using Alternative Proteases and Tandem Mass Tags. *Analytical Chemistry*, 2026

Gomes FP, ..., **Garrett PT**, et al. Native top-down proteomics enables discovery in endocrine-resistant breast cancer. *Nature Chemical Biology*, 2025

AWARDS & HONORS

Grand Prize, Scripps Research Hackathon (*Scripps Research*)

2026

Edgington Endowed Fellowship (*Skaggs Graduate School, Scripps Research*)

2022–2024